

SEQUENCE LISTING

SEQ ID NO: 1

MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCCLTVVSF
YQVAALQGD LASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPAPGEGNSSQNSRNK
RAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQ
VLYTDKTYAMGH LIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIP
RENAQISLDGDVTFFGALKLL

SEQ ID NO:2:

Leu	Glu	Arg	Cys	Arg	Tyr	Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu
1				5					10					15	
Glu	Ala	Arg	Ala	Cys	His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg
				20				25						30	
Thr	Gly	Phe	Phe	Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys
				35				40						45	
Pro	Pro	Gly	Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr
				50				55						60	
Gln	Cys	Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser
65					70					75					80
Ser	Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala
				85						90					95
Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser	Cys
				100						105					110
Thr	Gly	Phe	Pro	Leu	Ser	Thr	Arg	Val	Pro	Gly	Ala	Glu	Glu	Cys	Glu
				115						120					125
Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser	Ile	Lys	Arg
				130						135					140
Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu							
145															150

SEQ ID NO:3:

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
20 25 30
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
35 40 45
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
50 55 60
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
65 70 75 80
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
85 90 95
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
100 105 110
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
115 120 125
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
130 135 140
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
145 150 155 160
Thr Val Ser Ser Pro Arg Asp Thr Ala Val Ala Ala Val Ile Cys Ser
165 170 175
Ala Leu Ala Thr Val Leu Leu Ala Cys Ser Ser Cys Val Ser Ser Thr
180 185 190
Ala Arg Gly Ser Ser Trp Arg Arg Asn Pro Ala Val Ser Ser His Pro
195 200 205
Ser Val
210

SEQ ID NO:4:

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
20 25 30
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
35 40 45
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
50 55 60
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
65 70 75 80
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
85 90 95
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
100 105 110
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
115 120 125
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
130 135 140
Tyr Glu Pro His Cys Glu
145 150

10	20	30	40	50	60	70	80	90
MVQLTQQTEL	QSLRREVSRL	QGTGGPSQNG	EGYPWQSLPE	QSSDALEAWE	NGERSRKRRRA	VLTQKQKKQH	SVLHLVPINA	TSKDDSDVTE
100	110	120	130	140	150	160	170	180
VMWQPALRRG	RGLQAQGYGV	RIQDAGVYLL	YSQVLFQDVT	FTMGQVVSRE	GQGRQETLFR	CIRSMPSHPD	RAYNSCYSAG	VFHLHQGDIL
190	200							
SVIIPRARAK	LNLSPHGTFL	GFVKL						

SEQ ID NO:5

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SEQ ID NO: 6

ACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCCCACGCGTCCGAGAAGACTTTGAAATTCT
TACAAAACTGAAAGTGAAATGAGGAAGACAGATTGAGCAATCCAATCGGAGGGTAAATGCCAGCA
AACCTACTGTACAGTAGGGGTAGAGATGCAGAAAGGCAGAAAGGAGAAAATTCAGGATAACTCTCC
TGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAA
TGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGA
TGA CTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCCTAAGAAAAGAGAAGAAATGAAACT
GAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAA
GCTGTCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCA
GGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAA
GCTGCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTACCCGCGGGACT
GAAAACTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGC
CGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGAAACACC
AACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCT
AGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTATATA
TATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTC
CATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGAAACA
CTACCCAATAATTCCTGCTATTGAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTCCAATT
GCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGGTGCATTGAAA
CTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCCTCTTCTGTACCTCTAAGAAGA
AAGAATCTAACTGAAAATAC CAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 7:

CTGGAGCGCT GCCGCTACTG CAACGTCCTC TGCGGGGAGC GTGAGGAGGA GGCACGGGCT	60
TGCCACGCCA CCCACAACCG TGCCTGCCGC TGCCGCACCG GCTTCTTCGC GCACGCTGGT	120
TTCTGCTTGG AGCACGCATC GTGTCCACCT GGTGCCGGCG TGATTGCCCC GGGCACCCCC	180
AGCCAGAACA CGCAGTGCCA GCCGTGCCCC CCAGGCACCT TCTCAGCCAG CAGCTCCAGC	240
TCAGAGCAGT GCCAGCCCCA CCGCAACTGC ACGGCCCTGG GCCTGGCCCT CAATGTGCCA	300
GGCTCTTCCT CCCATGACAC CCTGTGCACC AGCTGCACTG GCTTCCCCCT CAGCACCAGG	360

GTACCAGGAG CTGAGGAGTG TGAGCGTGCC GTCATCGACT TTGTGGCTTT CCAGGACATC 420

TCCATCAAGA GGCTGCAGCG GCTGCTGCAG GCCCTCGAG 459

SEQ ID NO:8:

TCCGGCGCCG CGGGGCAGGA CAAGGGGAAG GAATAAACAC GTTTGGTGAG AGCCATGGCA 60

CTCAAGGTCC TACCTCTACA CAGGACGGTG CTCTTCGCTG CCATTCTCTT CCTACTCCAC 120

CTGGCATGTA AAGTGAGTTG CGAAACCGGA GATTGCAGGC AGCAGGAATT CAAGGATCGA 180

TCTGGAAACT GTGTCCTCTG CAAACAGTGC GGACCTGGCA TGGAGTTGTC CAAGGAATGT 240

GGCTTCGGCT ATGGGGAGGA TGCACAGTGT GTGCCCTGCA GGCCGCACCG GTTCAAGGAA 300

GACTGGGGTT TCCAGAAGTG TAAGCCATGT GCGGACTGTG CGCTGGTGAA CCGCTTTCAG 360

AGGGCCAACT GCTCACACAC CAGTGATGCT GTCTGCGGGG ACTGCCTGCC AGGATTTTAC 420

CGGAAGACCA AACTGGTTGG TTTTCAAGAC ATGGAGTGTG TGCCCTGCGG AGACCCACCT 480

CCTCCCTACG AACCACACTG TACCAGCAAG GTGAACCTTG TGAAGATCTC CTCCACCGTC 540

TCCAGCCCTC GGGACACGGC GGTGGCTGCC GTCATCTGCA GTGCTCTGGC CACGGTGCTG 600

CTCGCCTGCT CATCCTGTGT GTCATCTACT GCAAGAGGCA GTTCATGGAG AAGAAACCCA 660

GCTGTAAGCT CCCATCCCTC TGTCTCACTG TGAAGTGAGC TTGTTAGCAT TGTCACCCAA 720

GAGTTCTCAA GACACCTGGC TGAGACCTAA GACCTTTAGA GCATCAACAG CTACTTAGAA 780

TACAAGATGC AGGAAAACGA GCCTCTTCAG GAATCTCAGG GCCTCCTAGG GATGCTGGCA 840

AGGCTGTGAT GTCTCAAGGC TACCAGGAAA AAATAAAAGT TGTCTATACC CTA 893

SEQ ID NO:9:

GAGGCAAGAT TCGGCACGAG GCGGTTTGGC GCGGAAGTGC TACCAAGCTG CGGAAAGCGT	60
GAGTCTGGAG CACAGCACTG GCGAGTAGCA GGAATAAACA CGTTTGGTGA GAGCCATGGC	120
ACTCAAGGTC CTACCTCTAC ACAGGACGGT GCTCTTCGCT GCCATTCTCT TCCTACTCCA	180
CCTGGCATGT AAAGTGAGTT GCGAAACCGG AGATTGCAGG CAGCAGGAAT TCAAGGATCG	240
ATCTGGAAAC TGTGTCCTCT GCAAACAGTG CGGACCTGGC ATGGAGTTGT CCAAGGAATG	300
TGGCTTCGGC TATGGGGAGG ATGCACAGTG TGTGCCCTGC AGGCCGCACC GGTTC AAGGA	360
AGACTGGGGT TTCCAGAAGT GTAAGCCATG TGCGGACTGT GCGCTGGTGA ACCGCTTTCA	420
GAGGGCCAAC TGCTCACACA CCAGTGATGC TGTCTGCGGG GACTGCCTGC CAGGATTTTA	480
CCGGAAGACC AAAGTGGTTG GTTTTCAAGA CATGGAGTGT GTGCCCTGCG GAGACCCACC	540
TCCTCCCTAC GAACCACACT GTGAGTGATG TGCCAAGTGG CAGCAGACCT TTAAAAAAA	600
AAGAAAAAAA AACAAACAAA AAC	623

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10      20      30      40      50      60      70      80      90
CTTCCTAGAG GGACTGGAAC CTAATTCTCC TGAGGCTGAG GGAGGGTGA GGGTCTCAAG GCAACGCTGG CCCCACGACG GAGTGCCAGG
GAAGGATCTC CCTGACCTTG GATTAAGAGG ACTCCGACTC CCTCCCACT CCCAGAGTTC CGTTGCGACC GGGGTGCTGC CTCACGGTCC

100     110     120     130     140     150     160     170     180
AGCACTAACA GTACCCCTTAG CTTGCTTTCC TCCTCCCTCC TTTTATTTT CAAGTTCCTT TTTATTTCTC CTGCGTAAC AACCTTCTTC
TCGTGATTGT CATGGGAATC GAACGAAAGG AGGAGGGAGG AAAAATAAAA GTTCAAGGAA AAATAAAGAG GAACGCATTG TTGGAAGAAG

190     200     210     220     230     240     250     260     270
CCTTCTGCAC CACTGCCCCG ACCCTTACCC GCCCCGCCAC CTCCTTGCTA CCCCCTCTT GAAACCACAG CTGTTGGCAG GGTCCCCAGC
GGAAGACGTG GTGACGGGCA TGGGAATGGG CGGGGCGGTG GAGGAACGAT GGGGTGAGAA CTTTGGTGTG GACAACCGTC CCAGGGGTGC

280     290     300     310     320     330     340     350     360
TCATGCCAGC CTCATCTCCT TTCTTGCTAG CCCCCAAAGS SCTCCAGGCA ACATGGGGGG CCCAGTCAGA GAGCCGGCAC TCTCAGTTGC
AGTACGGTCG GAGTAGAGGA AAGAACGATC GGGGGTTTCS SGAGGTCCGT TGTACCCCCC GGGTCAGTCT CTCGGCCGTG AGAGTACACG

370     380     390     400     410     420     430     440     450
CCTCTGGTTG AGTTGGGGGG CAGCTCTGGG GGCCGTGSBT TGTGCATGGT YBAGCTGACC CAACAAACAG AGCTGCAGAS CCTCAGGAGA
GGAGACCAAC TCAACCCCCC GTCGAGACCC CCGGCACSVB ACACGTACCA RVTGCACTGG GTTGTGTTGC TCGACGTCTG GAGTCTCTCT

460     470     480     490     500     510     520     530     540
GAGGTGAGCC GGCTGCAGGG GACAGGAGGC CCTCCCAGA ATGGGGAAGG GTATCCCTGG CAGAGTCTCC CGGAGCAGAG TTCCGATGCC
CTCCACTCGG CCGACGTCCC CTGTCCTCCG GGGAGGGTCT TACCCCTTCC CATAGGGACC GTCTCAGAGG GCCTCGTCTC AAGGCTACGG

550     560     570     580     590     600     610     620     630
CTGGAAGCCT GGGAGAATGG GGAGAGATCC CGGAAAAGGA GAGCAGTGCT CACCCAAAAA CAGAAGAAGC AGCACTCTGT CCTGCACCTG
GACCTTCGGA CCTCTTACC CCTCTCTAGG GCCTTTTCTT CTCGTACGTA GTGGGTTTTT GTCTTCTCG TCGTGAGACA GGACGTGGAC

640     650     660     670     680     690     700     710     720
GTTCCCATTA ACGCCACCTC CAAGGATGAC TCCGATGTGA CAGAGGTGAT GTGGCAACCA GCTCTTAGGC GTGGGAGAGG CCTACAGGCC
CAAGGGTAAT TGCGGTGGAG GTTCTACTG AGGCTACACT GTCTCCACTA CACCGTTGGT CGAGAATCCG CACCCTCTCC GGATGTCCGG

730     740     750     760     770     780     790     800     810
CAAGGATATG GTGTCCGAAT CCAGGATGCT GGAGTTTATC TGCTGTATAG CCAGGTCTCTG TTCAAGACG TGACTTTTAC CATGGGTGAG
GTTCTATATC CACAGGCTTA GGTCTACGA CCTCAAATAG ACGACATATC GGTCCAGGAC AAAGTTCTGC ACTGAAAGTG GTACCCAGTC

820     830     840     850     860     870     880     890     900
GTGGTGTCTC GAGAAGGCCA AGGAAGGCAG GAGACTCTAT TCCGATGTAT AAGAAGTATG CCTTCCACC CGGACCGGGC CTACAACAGC
CACCACAGAG CTCTTCCGGT TCCTTCCGTC CTCTGAGATA AGGCTACATA TTCTTCATAC GGGAGGGTGG GCCTGGCCCG GATGTTGTGC

910     920     930     940     950     960     970     980     990
TGCTATAGCG CAGGTGCTTT CCATTTACAC CAAGGGGATA TTCTGAGTGT CATAATTCCC CGGGCAAGGG CGAAACTTAA CCTCTCTCCA
ACGATATCGC GTCCACAGAA GGTAAATGTG GTTCCCCTAT AAGACTCACA GTATTAAGGG GCCCGTTCCC GCTTTGAATT GGAGAGAGGT

1000    1010    1020    1030    1040    1050    1060    1070    1080
CATGGAACCT TCCTGGGGTT TGTGAACTG TGATTGTGTT ATAAAAAGTG GCTCCCAGCT TGGAAGACCA GGGTGGGTAC ATACTGGAGA
GTACCTTGGG AGGACCCCAA ACACTTTGAC ACTAACACAA TATTTTTCAC CGAGGGTCGA ACCTTCTGGT CCCACCCATG TATGACCTCT

1090    1100    1110    1120    1130    1140    1150    1160    1170
CAGCCAAGAG CTGAGTATAT AAAGGAGAGG GAATGTGCAG GAACAGAGGC ATCTTCTCTG GTTTGGCTCC CCGTTCCTCA CTTTTCCTTT
GTCGGTTCTC GACTCATATA TTCTCTCTCC CTTACACGTC CTTGTCTCCG TAGAAGGACC CAAACCGAGG GGCAAGGAGT GAAAAGGGAA

1180    1190    1200    1210    1220    1230    1240    1250    1260
TTCATTCCCA CCCCCTAGAC TTTGATTTTA CGGATATCTT GCTTCTGTTC CCGATGGAGC TCCGAATTCT TCGGTGTGTG TAGATGAGGG
AAGTAAGGGT GGGGGATCTG AACTAAAAAT GCCTATAGAA CGAAGACAAG GGTACCTCG AGGCTTAAGA ACGCACACAC ATCTACTCCC
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seq ID NO:10

SEQ ID NO:11

AGGTCCATGTCTTTGGG

SEQ ID NO:12

GGGGATGAATTGAGTCTG

SEQ ID NO:13

GTGCCCTCGAAGAAAAAG

SEQ ID NO:14

GCAAGTTGGAGTTCATC

SEQ ID NO:15

EYMPTD

SEQ ID NO:16

EYMPTE